

015745-9.ST25.txt
SEQUENCE LISTING

<110> LUKYANOV, SERGI A
SHAGIN, DMITRY A
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA
HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10/532,681
<141> 2005-04-26

<160> 22

<170> PatentIn version 3.3

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<212> DNA

<213> phialidium sp

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ggttatggag atgcaagtgt tggtaagtt gatgccaat tcattctgcac aactggagat 180
gtaccagttc catggtaac ttttagtaaca acacttactt atggcaca atgcttcgccc 240
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aaagaagact tcattgtgc agaccacacc caaatgaaca cacccattgg tggtgacca 600
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<400> 2

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015745-9.ST25.txt

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 3

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<212> DNA

<213> ARTIFICIAL SEQUENCE

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015745-9.ST25.txt

<223> phiYFP-Y1 mutant of the phiYFP

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gtaacaacac ttacttatgg tgccacaatgc ttcccaaatttgc atgggtccaga attaaaggat	240	
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atgacataacc atgtcactct cagcaaaagat gttactgatc acagggataaa catgagcttgatc	660	
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<213> ARTIFICIAL SEQUENCE

<220>

<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

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Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys			
35	40	45	

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu			
50	55	60	

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp			
65	70	75	80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile			
85	90	95	

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe			
		Page 3	

015745-9.ST25.txt
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
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Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 5
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<212> DNA
<213> ARTIFICIAL SEQUENCE

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aaagttgtatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300
gacggaaact ttaaaactcg cgctgaagtt acatggaaa acggatctgt ttataaccga 360
gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttgaaa gaatcttgaa 420
ttcaatttca cacctcattt tctttacatt tggggagatc aggctaattca tggtttgaag 480
tctgcttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttgcagac 540
cacacccaaa tgaacacacc cattgggtggt ggaccagtcc atgtccctga aaaccatcat 600

015745-9.ST25.txt

atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660
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<213> ARTIFICIAL SEQUENCE

<220>
<223> phiYFP-M0 mutant of the phiYFP

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

015745-9.ST25.txt

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 7
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<213> ARTIFICIAL SEQUENCE

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aaagttcatg cccaaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240
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gacggaaact ttaaaactcg cgctgaagtt acatttggaaa acggatctgt ttataaccga 360
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<213> ARTIFICIAL SEQUENCE

<220>
<223> phiYFP-M1 mutant of the phiYFP

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
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Glu Met Glu Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

015745-9.ST25.txt

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 9
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<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> humanized version of the phiYFP-M1

<400> 9

015745-9.ST25.txt

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gtgaccaccc	tgacctacgg	cgcccagtgc	ttcgccaagt	acggcccccga	gctgaaggat	240
ttctacaaga	gctgcatgcc	cgatggctac	gtgcaggagc	gcaccatcac	cttcgagggc	300
gatggcaatt	tcaagacccg	cgccgaggtg	accttcgaga	atggcagcgt	gtacaatcgc	360
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cacacccaga	tgaataacccc	catcggcgcc	ggccccgtgc	acgtgcccga	gtaccaccac	600
atgagctacc	acgtgaagct	gagcaaggat	gtgaccgatc	accgcgataa	tatgagcctg	660
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<213> ARTIFICIAL SEQUENCE

<220>
<223> humanized version of the phiYFP-M1

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20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

015745-9.ST25.txt

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

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<212> DNA
 <213> Anthomedusae species

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	ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaacccgt catacttggt	180
	gcaatgacag aaacatttca gaaaaatttgc ccatataagt tagaatttgc tggagatgtt	240
	gatggcaaaa catttaaggt tatttgttgc ggcgttgggg atgcaaccac tgggttaatt	300
	gaaggaaaaat atgtttgtac agaaggagaa gttccttattt catgggtttc gtcatcacc	360
	tcatattaatgtt atgggtgcgaa atgtttgtt cgtatccaa atgaaataaaa tgatttttc	420
	aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgtatgtt	480
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	cctccttcga caacatatgt tggcccgag ggagaaggta ttcgaatcat ctatagaaac	660
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015745-9.ST25.txt

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ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa 960
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<213> Anthomedusae species

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Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro
20 25 30

Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
35 40 45

Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
50 55 60

Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
65 70 75 80

Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
85 90 95

Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
100 105 110

Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
115 120 125

Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
130 135 140

Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
145 150 155 160

Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
165 170 175

015745-9.ST25.txt

Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
 180 185 190

Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
 195 200 205

Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala
 210 215 220

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp
 225 230 235 240

Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala
 245 250 255

Phe Asp Ala Asp Phe Ser
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<210> 13
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 <212> DNA
 <213> Anthomedusae species

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cattatttca atccgatatg acattcaaga tcttcatcga tggagtggtg aatgatcaga	240
aattcacat aatcgcagat ggatcgtcca aattccccca tggacttc aacgtgcatt	300
ctgtgtgcga aaccggaaaa ctcccaatgt catggaaacc tatttgcac cttatccaaat	360
acggggagcc attcttgca aaatatccca atggcatcag ccattttgca caggagtgt	420
ttccagaagg attaacaatt gatcgaacag tcagattcga aatgacggc actatgacgt	480
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015745-9.ST25.txt

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<212> PRT
<213> Anthomedusae species

<400> 14

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20 25 30

Gly Ser Ser Lys Phe Pro His Gln Asp Phe Asn Val His Ala Val Cys 45
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile 60
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His 80
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val 95
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu 110
100 105 110

Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe 125
115 120 125

Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro 140
130 135 140

Thr Glu Thr His Met Phe Pro His Gln Ser Asn Ala Val Arg Gln Leu 160
145 150 155 160

Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gln Gly Leu Met Met Ser His 175
165 170 175

Phe Asp Ser Lys Leu Thr Phe Asn Gln Ser Arg Ala Ile Lys Ile Pro 190
180 185 190

Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser 205
195 200 205

015745-9.ST25.txt

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 15
<211> 699
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> S3-2 mutant of hm2CP from a hydromedusa 2 of sub-order
Anthomedusa

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gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaaccatt 180
tgtcacctt tccaatacgg ggagccattc tttgcaagat atcccaacgg catcagccat 240
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gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgttccagg 360
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<211> 232
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> S3-2 mutant of hm2CP from a hydromedusa 2 of sub-order
Anthomedusae

<400> 16

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
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Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
20 25 30

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Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
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Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 17

<211> 705

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the
phiYFP-M1

<400> 17

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gtgaagctga	atggccaggg	cttcaagaag	gatggccacg	tgctgggcaa	gaatctggag	420
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agcgccttca	agatctgcca	cgagatcacc	ggcagcaagg	gcatgttcat	cgtggccgat	540
cacacccaga	tgaataacccc	catcggcggc	ggccccgtgc	acgtgcccga	gtaccaccac	600
atgagcaccc	acgtgaagct	gagcaaggat	gtgaccgatc	accgcgataa	tatgagcctg	660
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<213> ARTIFICIAL SEQUENCE

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<223> phiYFP-M1C1 mutant, derived from humanized version of the
phiYFP-M1

<400> 18

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Gly	Tyr	Gly	Asp	Ala	Ser	Val	Gly	Lys	Val	Asp	Ala	Gln	Phe	Ile	Cys
						35		40				45			

Thr	Thr	Gly	Asp	Val	Pro	Val	Pro	Trp	Ser	Thr	Leu	Val	Thr	Thr	Leu
					50					55		60			

Ser	Tyr	Gly	Ala	Gln	Cys	Phe	Ala	Lys	Tyr	Gly	Pro	Glu	Leu	Lys	Asp
					65			70		75		80			

Phe	Tyr	Lys	Ser	Cys	Met	Pro	Asp	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile
					85				90				95		

Thr	Phe	Glu	Gly	Asp	Gly	Asn	Phe	Lys	Thr	Arg	Ala	Glu	Val	Thr	Phe
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015745-9.ST25.txt

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
225 230

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cacacccaga tgaatacccc catcggcgac ggccccgtgc acgtgcccga gtaccaccac 600
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015745-9.ST25.txt

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 <223> phiYFP-M1C1 mutant, derived from humanized version of the
 phiYFP-M1

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
 180 185 190

015745-9.ST25.txt

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 21

<211> 699

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> humanized version of th S3-2 mutant of hm2cp from a hydromedusa
 2of sub-order Anthomedusae

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 gacttcaacg tgcacgcccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc 180
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 gacatcctgc ccaacgagac ccacatgttc cccacggcc ccaacgcccgt ggcgcagctg 480
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<210> 22

<211> 232

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> humanized S3-2 mutant of hm2cp from a hydromedusa 2 of sub-order
 Anthomedusae

<400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
 1 5 10 15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
 Page 18

20

25

30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230